

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Bandman, Olga
Hillman, Jennifer L.
Lal, Preeti
Corley, Neil C.
Shah, Purvi
- (ii) TITLE OF THE INVENTION: HUMAN RETICULOCALBIN ISOFORMS
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Hereewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0358 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650-855-0555
 - (B) TELEFAX: 650-845-4166
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 328 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: RATRNOT02
 - (B) CLONE: 922578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Met	Trp	Arg	Pro	Ser	Val	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	His
1				5					10					15	
Gly	Ala	Gln	Gly	Lys	Pro	Ser	Pro	Asp	Ala	Gly	Pro	His	Gly	Gln	Gly
			20					25					30		
Arg	Val	His	Gln	Ala	Ala	Pro	Leu	Ser	Asp	Ala	Pro	His	Asp	Asp	Ala
		35					40					45			
His	Gly	Asn	Phe	Gln	Tyr	Asp	His	Glu	Ala	Phe	Leu	Gly	Arg	Glu	Val
	50					55					60				
Ala	Lys	Glu	Phe	Asp	Gln	Leu	Thr	Pro	Glu	Glu	Ser	Gln	Ala	Arg	Leu
65					70					75				80	
Gly	Arg	Ile	Val	Asp	Arg	Met	Asp	Arg	Ala	Gly	Asp	Gly	Asp	Gly	Trp
			85						90					95	
Val	Ser	Leu	Ala	Glu	Leu	Arg	Ala	Trp	Ile	Ala	His	Thr	Gln	Gln	Arg
			100					105					110		
His	Ile	Arg	Asp	Ser	Val	Ser	Ala	Trp	Asp	Thr	Tyr	Asp	Thr	Asp	
	115						120				125				
Arg	Asp	Gly	Arg	Val	Gly	Trp	Glu	Glu	Leu	Arg	Asn	Ala	Thr	Tyr	Gly
	130					135					140				
His	Tyr	Ala	Pro	Gly	Glu	Glu	Phe	His	Asp	Val	Glu	Asp	Ala	Glu	Thr
145					150					155				160	
Tyr	Lys	Lys	Met	Leu	Ala	Arg	Asp	Glu	Arg	Phe	Arg	Val	Ala	Asp	
			165						170					175	
Gln	Asp	Gly	Asp	Ser	Met	Ala	Thr	Arg	Glu	Glu	Leu	Thr	Ala	Phe	Leu
			180					185					190		
His	Pro	Glu	Glu	Phe	Pro	His	Met	Arg	Asp	Ile	Val	Ile	Ala	Glu	Thr
	195						200					205			
Leu	Glu	Asp	Leu	Asp	Arg	Asn	Lys	Asp	Gly	Tyr	Val	Gln	Val	Glu	Glu
	210					215					220				
Tyr	Ile	Ala	Asp	Leu	Tyr	Ser	Ala	Glu	Pro	Gly	Glu	Glu	Glu	Pro	Ala
225					230					235				240	
Trp	Val	Gln	Thr	Glu	Arg	Gln	Gln	Phe	Arg	Asp	Phe	Arg	Asp	Leu	Asn
			245						250					255	
Lys	Asp	Gly	His	Leu	Asp	Gly	Ser	Glu	Val	Gly	His	Trp	Val	Leu	Pro
			260					265					270		
Pro	Ala	Gln	Asp	Gln	Pro	Leu	Val	Glu	Ala	Asn	His	Leu	Leu	His	Glu
		275					280					285			
Ser	Asp	Thr	Asp	Lys	Asp	Gly	Arg	Leu	Ser	Lys	Ala	Glu	Ile	Leu	Gly
	290				295						300				
Asn	Trp	Asn	Met	Phe	Val	Gly	Ser	Gln	Ala	Thr	Asn	Tyr	Gly	Glu	Asp
305				310						315				320	
Leu	Thr	Arg	His	His	Asp	Glu	Leu								
				325											

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: RATRNOT2
- (B) CLONE: 922578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGCAGAGCGG	ACGTGGAGAG	CGGACGNCAG	CTGGATAACA	GGGGACCGAT	GATGTGGCGA	60
CCATCAGTTC	TGCTGCTTCT	GTTGCTACTG	AGGCACGGGG	CCCAGGGGAA	GCCATCCCCA	120

GACGCAGGCC	CTCATGGCCA	GGGGAGGGTG	CACCAGGCGG	CCCCCCTGAG	CGACGCTCCC	180
CATGATGACG	CCCACGGGAA	CTTCCAGTAC	GACCATGAGG	CTTTCCTGGG	ACGGGAAGTG	240
GCCAAGGAAT	TCGACCAACT	CACCCCAGAG	GAAAGCCAGG	CCCGTCTGGG	GCGGATCGTG	300
GACCGCATGG	ACCGCGCGGG	GGACGGCGAC	GGCTGGGTGT	CGCTGGCCGA	GCTTCGCGCG	360
TGGATCGCGC	ACACGCAGCA	GCGGCACATA	CGGGACTCGG	TGAGCGCGGC	CTGGGACACG	420
TACGACACGG	ACCGCGACGG	GCGTGTGGGT	TGGGAGGAGC	TGCGCAACGC	CACCTATGGC	480
CACTACGCGC	CCGGTGAAGA	ATTTTCATGAC	GTGGAGGATG	CAGAGACCTA	CAAAAAGATG	540
CTGGCTCGGG	ACGAGCGGCG	TTTCCGGGTG	GCCGACCAGG	ATGGGGACTC	GATGGCCACT	600
CGAGAGGAGC	TGACAGCCTT	CCTGCACCCC	GAGGAGTTCC	CTCACATGCG	GGACATCGTG	660
ATTGCTGAAA	CCCTGGAGGA	CCTGGACAGA	AACAAAGATG	GCTATGTCCA	GGTGGAGGAG	720
TACATCGCGG	ATCTGTACTC	AGCCGAGCCT	GGGGAGGAGG	AGCCGGCGTG	GGTGCAGACG	780
GAGAGGCAGC	AGTTCCGGGA	CTTCCGGGAT	CTGAACAAGG	ATGGGCACCT	GGATGGGAGT	840
GAGGTGGGCC	ACTGGGTGCT	GCCCCCTGCC	CAGGACCAGC	CCCTGGTGGA	AGCCAACCAC	900
CTGCTGCACG	AGAGCGACAC	GGACAAGGAT	GGGCGGCTGA	GCAAAGCGGA	AATCCTGGGT	960
AATTGGAACA	TGTTTGTGGG	CAGTCAGGCC	ACCAACTATG	GCGAGGACCT	GACCCGGCAC	1020
CACGATGAGC	TGTGAGCACC	GCGCACCTGC	CACAGCCTCA	GAGGCCCGCA	CAATGACCGG	1080
AGGAGGGGCC	GCTGTGGTCT	GGCCCCCTCC	CTGTCCAGGC	CCCGCAGGAG	GCAGATGCAG	1140
TCCCAGGCAT	CCTCCTGCCC	CTGGGCTCTC	AGGGACCCCC	TGGGTCTGGCT	TCTGTCCCTG	1200
TCACACCCCC	AACCCAGGGG	AGGGGCTGTC	ATAGTCCCAG	AGGATAAGCA	ATACCTATTT	1260
CTGACTGAGT	CTCCCAGCCC	AGACCCAGGG	ACCCTTGGCC	CCAAGCTCAG	CTCTAAGAAC	1320
CGCCCCAACC	CCTCCAGCTC	CAAATCTGAG	CCTCCACCAC	ATAGACTGAA	ACTCCCCTGG	1380
CCCCAGCCCT	CTCCTGCCTG	GCCTGGCCTG	GGACACCTCC	TCTCTGCCAG	GAGGCAATAA	1440
AAGCCAGCGC	CGGGAAAAAA	AAA				1463

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADNOT03
- (B) CLONE: 1601793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Asp	Leu	Arg	Gln	Phe	Leu	Met	Cys	Leu	Ser	Leu	Cys	Thr	Ala	Phe
1				5				10						15	
Ala	Leu	Ser	Lys	Pro	Thr	Glu	Lys	Lys	Asp	Arg	Val	His	His	Glu	Pro
			20					25					30		
Gln	Leu	Ser	Asp	Lys	Val	His	Asn	Asp	Ala	Gln	Ser	Phe	Asp	Tyr	Asp
		35					40					45			
His	Asp	Ala	Phe	Leu	Gly	Ala	Glu	Glu	Ala	Lys	Thr	Phe	Asp	Gln	Leu
	50				55						60				
Thr	Pro	Glu	Glu	Ser	Lys	Glu	Arg	Leu	Gly	Lys	Ile	Val	Ser	Lys	Ile
65				70						75				80	
Asp	Gly	Asp	Lys	Asp	Gly	Phe	Val	Thr	Val	Asp	Glu	Leu	Lys	Asp	Trp
			85						90					95	
Ile	Lys	Phe	Ala	Gln	Lys	Arg	Trp	Ile	Tyr	Glu	Asp	Val	Glu	Arg	Gln
			100					105					110		
Trp	Lys	Gly	His	Asp	Leu	Asn	Glu	Asp	Gly	Leu	Val	Ser	Trp	Glu	Glu
		115				120						125			
Tyr	Lys	Asn	Ala	Thr	Tyr	Gly	Tyr	Val	Leu	Asp	Asp	Pro	Asp	Pro	Asp
	130					135					140				
Asp	Gly	Phe	Asn	Tyr	Lys	Gln	Met	Met	Val	Arg	Asp	Glu	Arg	Arg	Phe
145				150						155				160	
Lys	Met	Ala	Asp	Lys	Asp	Gly	Asp	Leu	Ile	Ala	Thr	Lys	Glu	Glu	Phe
			165					170						175	

Thr Ala Phe Leu His Pro Glu Glu Tyr Asp Tyr Met Lys Asp Ile Val
 180 185 190
 Val Gln Glu Thr Met Glu Asp Ile Asp Lys Asn Ala Asp Gly Phe Ile
 195 200 205
 Asp Leu Glu Glu Tyr Ile Gly Asp Met Tyr Ser His Asp Gly Asn Thr
 210 215 220
 Asp Glu Pro Glu Trp Val Lys Thr Glu Arg Glu Gln Phe Val Glu Phe
 225 230 235 240
 Arg Asp Lys Asn Arg Asp Gly Lys Met Asp Lys Glu Glu Thr Lys Asp
 245 250 255
 Trp Ile Leu Pro Ser Asp Tyr Asp His Ala Glu Ala Glu Ala Arg His
 260 265 270
 Leu Val Tyr Glu Ser Asp Gln Asn Lys Asp Gly Lys Leu Thr Lys Glu
 275 280 285
 Glu Ile Val Asp Lys Tyr Asp Leu Phe Val Gly Ser Gln Ala Thr Asp
 290 295 300
 Phe Gly Glu Ala Leu Val Arg His Asp Glu Phe
 305 310 315

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2658 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADNOT03
 (B) CLONE: 1601793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCCGCTTCCG	GTTGGGCGGT	GCTTGCGCGC	GTGAGCTGAG	CCGGTGGGGT	AGCGGCGGCC	60
ACGGCATCCT	GTGCTGTGGG	GGCTACGAGG	AAAGATCTAA	TTATCATGGA	CCTGCGACAG	120
TTTCTTATGT	GCCTGTCCCT	GTGCACAGCC	TTTGCCTTGA	GCAAACCCAC	AGAAAAGAAG	180
GACCGTGTAC	ATCATGAGCC	TCAGCTCAGT	GACAAGGTTT	ACAATGATGC	TCAGAGTTTT	240
GATTATGACC	ATGATGCCTT	CTTGGGTGCT	GAAGAAGCAA	AGACCTTTGA	TCAGCTGACA	300
CCAGAAGAGA	GCAAGGAAAG	GCTTGGAAAG	ATTGTAAGTA	AAATAGATGG	CGACAAGGAC	360
GGGTTTGTCA	CTGTGGATGA	GCTCAAAGAC	TGGATTAAAT	TTGCACAAAA	GCGCTGGATT	420
TACGAGGATG	TAGAGCGACA	GTGGAAGGGG	CATGACCTCA	ATGAGGACGG	CCTCGTTTCC	480
TGGGAGGAGT	ATAAAAATGC	CACCTACGGC	TACGTTTTAG	ATGATCCAGA	TCCTGATGAT	540
GGATTTAAC	ATAAACAGAT	GATGGTTAGA	GATGAGCGGA	GGTTTAAAT	GGCAGACAAG	600
GATGGAGACC	TCATTGCCAC	CAAGGAGGAG	TTACACAGCT	TCCTGCACCC	TGAGGAGTAT	660
GACTACATGA	AAGATATAGT	AGTACAGGAA	ACAATGGAAG	ATATAGATAA	GAATGCTGAT	720
GGTTTCATTG	ATCTAGAAGA	GTATATTGGT	GACATGTACA	GCCATGATGG	GAATACTGAT	780
GAGCCAGAAT	GGGTAAAGAC	AGAGCGAGAG	CAGTTTGTG	AGTTTCGGGA	TAAGAACCGT	840
GATGGGAAGA	TGGACAAGGA	AGAGACCAAA	GACTGGATCC	TTCCCTCAGA	CTATGATCAT	900
GCAGAGGCAG	AAGCCAGGCA	CCTGGTCTAT	GAAATCAGACC	AAAACAAGGA	TGGCAAGCTT	960
ACCAAGGAGG	AGATCGTTGA	CAAGTATGAC	TTATTTGTG	GCAGCCAGGC	CACAGATTTT	1020
GGGGAGGCCT	TAGTACGGCA	TGATGAGTTC	TGAGCTACGG	AGGAACCTC	ATTTCCCTCA	1080
AAGTAATTTA	TTTTTACAGC	TTCTGGTTTC	ACATGAAATT	GTTTGCCTA	CTGAGACTGT	1140
TACTACAAAC	TTTTTAAGAC	ATGAAAAGGC	GTAATGAAA	CCATCCCGTC	CCCATTCCCT	1200
CTCCTCTCTG	AGGGACTGGA	GGGAAGCCGT	GCTTCTGAGG	AACAACCTA	ATTAGTACAC	1260
TTGTGTTTGT	AGATTTACAC	TTGTATTAT	GATTTAAGAT	GGCGTGTTTA	TTTTTGTATT	1320
TTTCTCTGGT	TGGGAGTATG	ATATGAAGGA	TCAAGATCCT	CAACTCACAC	ATGTAGACAA	1380
ACATTAGCTC	TTTACTCTTT	CTCAACCCCT	TTTATGATTT	TAATAATTCT	CACTTAACCTA	1440
ATTTTGTAAG	CCTGAGATCA	ATAAGAAATG	TTCAGGAGAG	AGGAAAGAAA	AAAAATATAT	1500
GCTCCACAAT	TTATATTTAG	AGAGAGAACA	CTTAGTCTTG	CCTGTCAAAA	AGTCCAACAT	1560
TTCATAGGTA	GTAGGGGCCA	CATATTACAT	TCAGTTGCTA	TAGGTCCAGC	AACTGAACCT	1620
GCCATTACCT	GGGCAAGGAA	AGATCCCTTT	GCTCTAGGAA	AGCTTGGCCC	AAATTGATTT	1680

TCTTCTTTTT	CCCCCTGTAG	GACTGACTGT	TGGCTAATTT	TGTCAAGCAC	AGCTGTGGTG	1740
GGAAGAGTTA	GGGCCAGTGT	CTTGAAAATC	AATCAAGTAG	TGAATGTGAT	CTCTTTGCAG	1800
AGCTATAGAT	AGAAACAGCT	GGAAAACATA	AGGAAAAATA	CAAATGTTTT	CGGGGCATAC	1860
ATTTTTTTTC	TGGGTGTGCA	TCTGTTGAAA	TGCTCAAGAC	TTAATTATTT	GCCTTTTGAA	1920
ATCACTGTAA	ATGCCCCCAT	CCGGTTCCTC	TTCTTCCCAG	GTGTGCCAAG	GAATTAATCT	1980
TGGTTTCACT	ACAATTAAAA	TTCACCTCCT	TCCAATCATG	TCATTGAAAG	TGCCTTTAAC	2040
GAAAGAAATG	GTCACCTGAAT	GGGAATTCTC	TTAAGAAACC	CTGAGATTAA	AAAAAGACTA	2100
TTTGGATAAC	TTATAGGAAA	GCCTAGAACC	TCCCAGTAGA	GTGGGGATTT	TTTTCTTCTT	2160
CCCTTTCCTT	TTTGGACAAT	AGTTAAATTA	GCAGTATTAG	TTATGAGTTT	GGTTGCAGTG	2220
TTCTTATCTT	GTGGGCTGAT	TTCCAAAAAC	CACATGCTGC	TGAATTTACC	AGGGATCCTC	2280
ATACCTCACA	ATGCAAACCA	CTTACTACCA	GGCCTTTTTT	TGTGTCCACT	GGAGAGCTTG	2340
AGCTCACACT	CAAAGATCAG	AGGACCTACA	GAGAGGGCTC	TTTGGTTTGA	GGACCATGGC	2400
TTACCTTTCC	TGCCTTTGAC	CCATCACACC	CCATTTCCCT	CTCTTTCCCT	CTCCCCGCTG	2460
CCAAAAAATA	AAAAAAGGA	AACGTTTATC	ATGAATCAAC	AGGGTTTCAG	TCCTTATCAA	2520
AGAGAGATGT	GGAAAGAGCT	AAAGAAACCA	CCCTTTGTTC	CCAACCTCCAC	TTTACCCATA	2580
TTTATGCAA	CACAAACACT	GTCCTTTTGG	GTCCCTTTCT	TACAGATGGG	ACCTCTTGAG	2640
GAAGGAATTA	TCGTATTC					2658

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1262329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ala	Arg	Gly	Gly	Arg	Gly	Arg	Arg	Leu	Gly	Leu	Ala	Leu	Gly	Leu
1				5					10					15	
Leu	Leu	Ala	Leu	Val	Leu	Ala	Pro	Arg	Val	Leu	Arg	Ala	Lys	Pro	Thr
			20					25					30		
Val	Arg	Lys	Glu	Arg	Val	Val	Arg	Pro	Asp	Ser	Glu	Leu	Gly	Glu	Arg
		35					40					45			
Pro	Pro	Glu	Asp	Asn	Gln	Ser	Phe	Gln	Tyr	Asp	His	Glu	Ala	Phe	Leu
	50				55					60					
Gly	Lys	Glu	Asp	Ser	Lys	Thr	Phe	Asp	Gln	Leu	Thr	Pro	Asp	Glu	Ser
65					70				75					80	
Lys	Glu	Arg	Leu	Gly	Lys	Ile	Val	Asp	Arg	Ile	Asp	Asn	Asp	Gly	Asp
			85					90					95		
Gly	Phe	Val	Thr	Thr	Glu	Glu	Leu	Lys	Thr	Trp	Ile	Lys	Arg	Val	Gln
			100				105					110			
Lys	Arg	Tyr	Ile	Phe	Asp	Asn	Val	Ala	Lys	Val	Trp	Lys	Asp	Tyr	Asp
	115					120					125				
Arg	Asp	Lys	Asp	Asp	Lys	Ile	Ser	Trp	Glu	Glu	Tyr	Lys	Gln	Ala	Thr
	130				135						140				
Tyr	Gly	Tyr	Tyr	Leu	Gly	Asn	Pro	Ala	Glu	Phe	His	Asp	Ser	Ser	Asp
145				150					155					160	
His	His	Thr	Phe	Lys	Met	Leu	Pro	Arg	Asp	Glu	Arg	Arg	Phe	Lys	
			165					170					175		
Ala	Ala	Asp	Leu	Asn	Gly	Asp	Leu	Thr	Ala	Thr	Arg	Glu	Glu	Phe	Thr
			180				185					190			
Ala	Phe	Leu	His	Pro	Glu	Glu	Phe	Glu	His	Met	Lys	Glu	Ile	Val	Val
	195					200					205				
Leu	Glu	Thr	Leu	Glu	Asp	Ile	Asp	Lys	Asn	Gly	Asp	Gly	Phe	Val	Asp
	210				215						220				

Gln	Asp	Glu	Tyr	Ile	Ala	Asp	Met	Phe	Ser	His	Glu	Glu	Asn	Gly	Pro
225					230					235					240
Glu	Pro	Asp	Trp	Val	Leu	Ser	Glu	Arg	Glu	Gln	Phe	Asn	Glu	Phe	Arg
				245					250					255	
Asp	Leu	Asn	Lys	Asp	Gly	Lys	Leu	Asp	Lys	Asp	Glu	Ile	Arg	His	Trp
		260					265					270			
Ile	Leu	Pro	Gln	Asp	Tyr	Asp	His	Ala	Gln	Ala	Glu	Ala	Arg	His	Leu
		275					280					285			
Val	Tyr	Glu	Ser	Asp	Lys	Asn	Lys	Asp	Glu	Lys	Leu	Thr	Lys	Glu	Glu
	290					295					300				
Ile	Leu	Glu	Asn	Trp	Asn	Met	Phe	Val	Gly	Ser	Gln	Ala	Thr	Asn	Tyr
305				310						315					320
Gly	Glu	Asp	Leu	Thr	Lys	Asn	His	Asp	Glu	Leu					
			325						330						

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 780361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg	Arg	Asp	Val	Ala	Lys	Glu	Phe	Asp	Gln	Leu	Thr	Pro	Glu	Glu	Ser
1				5					10					15	
Gln	Ala	Arg	Leu	Gly	Arg	Ile	Val	Asp	Arg	Met	Asp	Leu	Ala	Gly	Asp
			20					25					30		
Ser	Asp	Gly	Trp	Val	Ser	Leu	Ala	Ala	Leu	Arg	Ala	Trp	Ile	Ala	His
		35				40						45			
Thr	Gln	Gln	Arg	His	Ile	Arg	Asp	Ser	Val	Ser	Ala	Ala	Trp	His	Thr
	50					55					60				
Tyr	Asp	Thr	Asp	Arg	Asp	Gly	Arg	Val	Gly	Trp	Glu	Glu	Leu	Arg	Asn
65					70					75					80
Ala	Thr	Tyr	Gly	His	Tyr	Glu	Pro	Gly	Glu	Glu	Phe	His	Asp	Val	Glu
				85					90					95	
Gly	Pro														